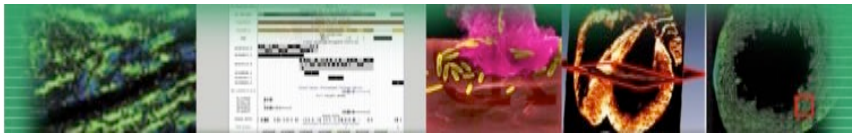
Writing/Speaking Support for 20.109



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Macrostructure of a Research Article

- ***Introduction*** provides general field or context.
- ***Methods*** follows a particularized path.
- ***Discussion*** moves from specific findings to wider implications.

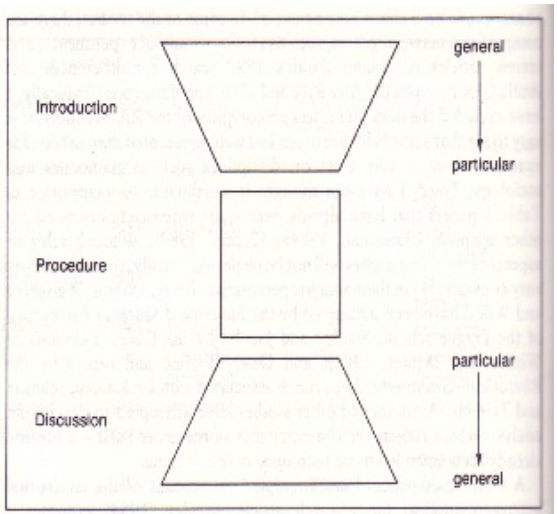
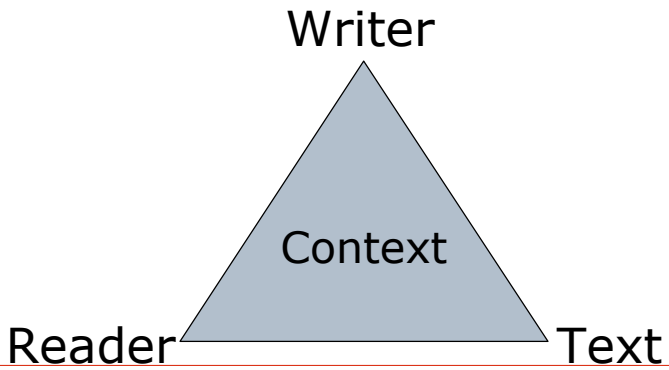


Figure 7 Overall organization of the research paper (Hill et al., 1982).

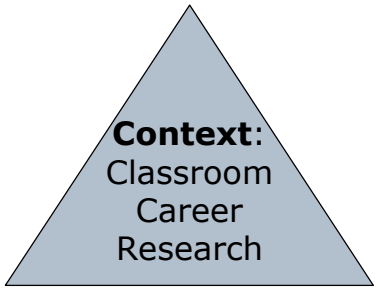
Writing and Thinking Rhetorically about Science

Any writing act can be described in terms of a rhetorical triangle or set of relationships.



The rhetorical relationships for scientific writing can be complex and shifting.

Writer/Student/Professional/Scientist



Reader:
Teacher
Research partner
Scientific community

Text: scientific data, the "story" of your findings

Scientific writers need to control the rhetoric of scientific writing.

According to Aristotle, rhetoric is "the art of finding in any given case the available means of persuasion."

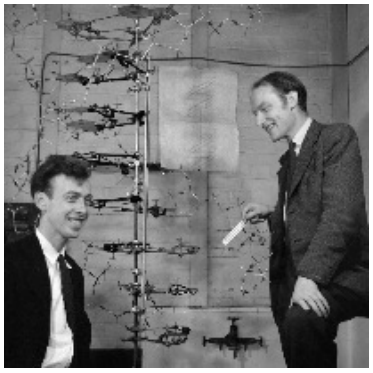
Writing and research are complex processes enabled by language.

"Language, oral or written, is an expressive instrument through which we communicate what we have previously thought [or discovered]. It is also the reflective instrument through which we think, alone or with others, about what we are doing." Paul Connolly

The goal of scientific writing is to court your audience.

Michael Halloran on Watson & Crick's 1953 "The Structure for DNA"

"The April 1953 paper, then, is really just the initial move in a rhetorical strategy aimed at gaining and holding the attention of an audience. As such, it presumes an understanding of *science as a human community* in which neither facts nor ideas speak for themselves, and the attention of the audience must be courted."



Research article scramble

- For the passages from a student!s 20.109 laboratory report on homologous recombination: Which section (Introduction, Methods, Results, Discussion, Figure Captions) does each passage belongs to?

1.0 Introduction

By obtaining a more profound understanding of all aspects of DNA repair pathways, it may be easier for future breakthroughs in creating chemotherapeutic strategies that specifically and effectively attack cancers, and thus radically change modern cancer treatment. In order to contribute to this understanding of homologous recombination, we have created an assay that will enable us to determine when homologous recombination has taken place.

What features of this paragraph identify it as belong to the Introduction?

From http://openwetware.org/wiki/20.109(S09):Protein_engineering_research_article

The introduction provides a framework for the story you are about to tell (The Amazing Adventures of a Mutant Calcium Sensor), and thus serves two main purposes. For one, you must provide **sufficient background information** for a reader to understand the forthcoming results. Just as importantly, you must **motivate the audience** to keep reading! How? **Reveal the significance** of the work through connections to both prior scientific accomplishments and future applications.

The Introduction establishes *context*, *focus*, and *justification*.

Context: Orient your reader to the published literature related to the topic and to essential background information

Focus: Define the research space, stake out territory. What questions are you addressing? What is your hypothesis?

Justification: Show how your work fits into and extends previous work. Argue for the importance of your work.

Swales (1990)

2.0 Methods

In order to perform bacterial transformation, 5 µl of each purification ligation reaction was added to 50 µl of competent bacterial cells, also a positive control was prepared with an uncut pCX-EGFP plasmid. These solutions were then heat shocked in a 42ºC bath for 90 seconds so that the competent cells could uptake the DNA. 0.5 ml of LB media was then added to each reaction, and 200 µl of each tube was plated onto separate LB + AMP plates using a sterile spreader. Each plate was then incubated at 37ºC overnight.

What features of this paragraph identify it as belong to the Materials & Methods?

From http://openwetware.org/wiki/20.109(S09):Protein_engineering_research_article

The methods section should allow an independent investigator **to repeat** some or all of your experiments. Use sub-section headings to allow readers to quickly identify experiments of interest to them. When commercially available kits were used, it is sufficient to cite the name of the kit and say that it was used according to the manufacturer's protocol. The key to a good methods section is developing your judgment for what information is essential and what is extraneous. [Note: Methods sections are generally **in past tense** as the work is done, completed, over!]

Your research article should contain a Methods Section, not a Protocol.

A Protocol is . . .

- A series of steps to be carried out.
- Written in sequential or temporal order.
- Intended for the reader to achieve a final result.

A Methods Section is

- A series of steps already completed and is written in past tense.
- Written in logical order.
- Intended for the reader to replicate the experiment.

3.0 Results

As expected the digestion of plasmid backbone (Lane 2) displayed a band of about 4.8 kbp in length, as digesting with SalI would linearize the DNA. However, two other bands were seen in addition to the expected band, which could be due to poor enzyme efficiency. Lanes 3-5 in Figure 6 also confirm the projected length fragments of 3.7 kbp and 1.6 kbp (from Figure 5). This result indicates that the candidate clones were indeed the desired construct.

What features of this paragraph identify it as belong to the Results?

From http://openwetware.org/wiki/20.109(S09):Protein_engineering_research_article

The purpose of the results section is **to present your data in a relatively unbiased way**, **but with some guiding framework**. Begin with a short overview of the entire experiment, and then delve into specific sub-sections that describe each piece of the work. Note that the sub-sections should be organized by functional content, not by what you did each day in lab. One potential division might be the following: construction of the mutant plasmid, verification of mutant DNA and protein production, and characterization of the mutant protein. However, other schemes could work as well or better.

Each sub-section should begin with an overview sentence that introduces the present experiment and end with a sentence stating the primary conclusion reached from that experiment. The overview and/or concluding sentences should also provide a transition to the previous/next piece of data. You may present your reader with the broad strokes of what your data indicate, particularly in the sub-section headings and concluding sentences, and in the figure caption titles. However, **you should reserve detailed interpretation of your data for the discussion section**.

What Differentiates Results from the Methods?

Methods = *How* the data were accumulated.

Results = *What* data were accumulated.

Readers expect to find the "answers" to your research questions in your Results section.

What Differentiates Results from Discussion?

Results = *Data Presentation*

("Experiments showed that . . . .")

Discussion = *Data Interpretation*

("Experiments suggest that . . . .")

However, you still need to choose which data to present in your Results Section (an act of interpretation!).

4.0 Figure Caption

Results of gel electrophoresis on 1% agarose gel. Lane 1-4 contain the pCX-NNX backbone. In Lane 1 the vector is uncut. In Lane 2 the plasmid is cut with XbaI (? 4.8 kbp), while in Lane 3 it is cut with EcoRI (? 4.8 kbp). Lane 4 shows the backbone double digest with XbaI and EcoRI (?4.7kbp). Lane 5 is the 10Kb DNA Ladder. Lanes 6-7 contain the ?5-EGFP (PCR Product) insert. Lane 6 is the double digest (?0.66 kp), and Lane 7 shows the uncut insert. Lane 8 is the negative PCR-no template control. (Yellow Group W/F)

What features of this paragraph identify it as belong to a Figure caption?

http://openwetware.org/wiki/20.109(S09):Guidelines_for_writing_up_your_research

Some readers begin by scanning the figures first. The figures, with the legends [or captions], should provide **a self-explanatory overview of your data**. Decide what the data show, then create figures which highlight the most important points of your paper. . . . Legends to the figures and tables explain the elements that appear in the illustration. . . . **Make sure each element of the figure or table is explained**. Your figure legends should be written in the present tense since you are explaining elements that still exist at the time that you are writing the paper.

Titles and captions allow figures and tables to stand on their own.

- **Guide** the reader to what is most important in the figure.
- **Contextualize** the data shown in terms of purpose and method.
- **Focus attention** on certain findings (e.g., relationship between values).
- **Summarize** the larger point.

Bonus tip!! Titles of tables go on TOP of the table while titles/captions of figures come BELOW the figure.

Connecting Results to Figures

From Kuroita, et al. "Structural mechanism for coordination of proofreading and polymerase activities in archael DNA polymerases." *JMB* 351, 2005, 291-298.

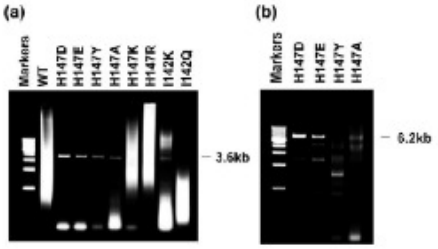


Figure 3. PCR with KOD polymerase mutants. (a) Agarose gel (1%) showing 3.6 kb PCR products. One unit of each mutant or WT enzyme was added to a mixture of 10 ng human genomic DNA and a primer pair designed to yield a 3.6 kb DNA fragment. (b) Long PCR with each mutant. One unit of each mutant was added to a mixture of 50 ng human genomic DNA and a primer pair designed to yield a 6.2 kb DNA fragment.

At first, a fragment of the human β-globin gene (3.6 kb) was amplified from different concentrations of human genomic DNA (final concentrations 2 ng/μl and 0.2 ng/μl) by each mutated enzyme. Under the high template DNA condition (2 ng/μl), each mutant showed a distinct band at the expected position upon gel analysis (data not shown). The change in template concentration from 2 ng/μl to 0.2 ng/μl greatly increased the frequency of failed reactions. Only four mutants (i.e. H147D, H147E, H147Y and H147A) resulted in successful amplification. Although I142K also showed a faint band, conspicuous unexpected bands were amplified at the same time. The other mutants generated only indistinct non-specific bands (Figure 3(a)). This experiment indicates that the 3′-5′exonuclease activity is not the only cause of PCR failure, because some mutants exhibiting similar Exo/Pol ratios (e.g. H147E and I142Q) produced different results. From these experiments, it is concluded that the negative charge or hydrophobicity of the amino acid at position 147 plays an important role for the sensitivity of PCR.

Next, the mutants that showed successful amplification in the above experiments (H147D, H147E, H147Y and H147A) were applied to "long PCR". A DNA fragment of the myosin heavy chain (6.2 kb) was amplified from human genomic DNA (final concentration, 1 ng/μl). As shown in Figure 3(b), H147D and H147E successfully amplified 6.2 kb products. The yield with H147D was higher than that with H147E. The target was not amplified by H147Y and H147A. PCR with the other mutants and the WT enzyme also ended in failure (data not shown). These results indicate that a negative charge at residue 147 of KOD DNA

5.0 Discussion

With regards to the results obtained from flow cytometry, several unexpected results were observed. To begin with, all the negative controls had some cells that fell to the right of the diagonal line (greater FL1:FL2 ratio), suggesting that they expressed EGFP. This is likely due to the MES cells having background fluorescence or that there was contamination in the samples. However the most surprising result was the almost complete lack of homologous recombination in the ?3+?5SgrAI samples. This was surprising as we hypothesized that an increase in distance of a double strand break would decrease HR; however, we still believed that it would be greater than having no double strand breaks.

What features of this paragraph identify it as belong to the Discussion?

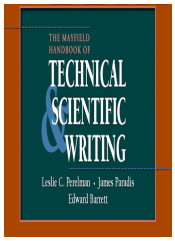
From http://openwetware.org/wiki/20.109(S09):Protein_engineering_research_article

The purpose of the discussion section is to **interpret and contextualize your data**. You should **begin by reiterating your major findings**. Then you might do any or all of the following: connect your findings to other research (published or that of your peers); describe any ambiguities and sources of error in the data, and suggest future experiments to resolve uncertainties; explain where you expect your work may lead, and suggest specific experiments for extending your findings; describe any conceptual or technical limitations of the research. Finally, you should **explain the significance of your findings to basic science and to engineering applications**. Like the previous sections, the discussion should have a clear organization and narrative flow.

What are the Pitfalls of a Discussion Section?

- Lack of **a "story"** of how you have interpreted your results.
- Does not start with context or reiteration of **key results**.
- Including **too much information** (wordy arguments, not focused, meandering, etc.).
- **Failure to follow** arguments set up in the **introduction**.
- **Failure to** focus on the **current results.**
- **Speculating** too much or not enough.
- **Improper tense:** Discussion is largely in present tense.
- **Hedging** excessively--don't be too tentative!

Good MIT Resources



The Mayfield Guide On-Line

http://www.mhhe.com/mayfieldpub/tsw/home.htm

The MIT Writing and Communication Center

Room 12-132; 617/253-3090

Appointments can be made from http://web.mit.edu/writing/.

Writing Resources on the 20.109 Wiki